

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

5 &lt;120&gt; Novel human G-protein coupled receptor

&lt;130&gt; SPW99.04

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 18

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 1659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36)..(1559)

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Asn Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu Ser  
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aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149  
Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu  
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gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197  
Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu  
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gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245  
Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile  
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ttt aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293  
Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro  
75 80 85

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tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341  
Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His  
90 95 100

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	ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc	389
	Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser	
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5	gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc	437
	Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile	
	120 125 130	
10	cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg	485
	His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu	
	135 140 145 150	
15	ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca	533
	Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro	
	155 160 165	
20	ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc	581
	Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys	
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25	tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtg gtg	629
	Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val	
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	Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val	
	200 205 210	
35	gtg ttc tgt gca gcc cgg agg cag cat gct ctg ctg tac aat gtc aag	725
	Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys	
	215 220 225 230	
40	aga cac agc ttg gaa gtg cga gtc aag gac tgt gtg gag aat gag gat	773
	Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp	
	235 240 245	
45	gaa gag gga gca gag aag aag gag gag ttc cag gat gag agt gag ttt	821
	Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe	
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	Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu	
	265 270 275	
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	Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser	
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	Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser	
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	Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys	
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gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac 1061  
 Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn  
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 cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac 1109  
 Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp  
 345 350 355  
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 gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag 1157  
 Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu  
 360 365 370  
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 agc ctc cca ccc agt cgt cgt aac agc aac agc aac cct cct ctg ccc 1205  
 Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro  
 375 380 385 390  
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 agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc 1253  
 Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe  
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 tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc 1301  
 Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala  
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 gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata 1349  
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 Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr  
 440 445 450  
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 ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag 1445  
 Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys  
 455 460 465 470  
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 Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp  
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 Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr  
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Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly  
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Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln  
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Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln  
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Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe  
 85 90 95

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Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His  
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Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp  
 115 120 125

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Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr  
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Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile  
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Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp  
 165 170 175

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Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr  
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Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met  
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Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala  
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Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp  
 225 230 235 240

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe  
 245 250 255

55

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Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala  
 260 265 270  
 5 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu  
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 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu  
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 10 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly  
 305 310 315 320  
 Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys  
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 Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly  
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 Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn  
 370 375 380  
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 385 390 395 400  
 30 Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys  
 405 410 415  
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 35 Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys  
 435 440 445  
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